

## SEQUENCE LISTING

<110> Debinski, Waldemar  
Thompson, Jeffrey

<120> IL13 MUTANTS

<130> 6460-28

<140> US 09/679,710

<141> 2000-10-05

<160> 23

<170> PatentIn version 3.0

<210> 1

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
100 105 110

Phe Asn

<210> 2

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<221> misc\_feature

<223> hIL13 mutant having a Glu to Lys substitution at residue 13

<400> 2

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu  
1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
100 105 110

Phe Asn

<210> 3

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; hIL13 mutant having a Glu to Ile substitution at residue 13

&lt;400&gt; 3

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ile Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

&lt;210&gt; 4

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; hIL13 mutant having a Glu to Cys substitution at residue 13

&lt;400&gt; 4

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Cys Leu Ile Glu

1            5            10            15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
20            25            30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
35            40            45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
50            55            60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
65            70            75            80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
85            90            95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
100            105            110

Phe Asn

<210> 5

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<221> misc\_feature

<223> hIL13 mutant having a Glu to Ser substitution at residue 13

<400> 5

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ser Leu Ile Glu  
1            5            10            15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
20            25            30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
35            40            45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 6

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<221> misc\_feature

<223> hIL13 mutant having a Glu to Arg substitution at residue 13

<400> 6

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Arg Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 7

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<221> misc\_feature

<223> hIL13 mutant having a Glu to Tyr substitution at residue 13

<400> 7

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Tyr Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 8

<211> 114  
 <212> PRT  
 <213> ARTIFICIAL SEQUENCE

<220>  
 <221> misc\_feature  
 <223> hIL13 mutant having a Glu to Asp substitution at residue 13

<400> 8

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Asp Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 9  
 <211> 114  
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<220>  
 <221> misc\_feature  
 <223> hIL13 mutant having a Glu to Lys substitution at residue 16

&lt;400&gt; 9

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Lys  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

&lt;210&gt; 10

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; hIL13 mutant having a Glu to Lys substitution at residue 17

&lt;400&gt; 10

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Lys Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30



Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 11

<211> 114

<212> PRT

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<221> misc\_feature

<223> hIL13 mutant having a Arg to Asp substitution at residue 66

<400> 11

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Asp Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln

65            70            75            80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
          85            90            95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
          100            105            110

Phe Asn

<210> 12

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<221> misc\_feature

<223> hIL13 mutant having a Ser to Asp substitution at residue 69

<400> 12

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
1            5            10            15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
          20            25            30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
          35            40            45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
          50            55            60

Gln Arg Met Leu Asp Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
65            70            75            80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
          85            90            95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
          100            105            110

Phe Asn

<210> 13

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<221> misc\_feature

<223> hIL13 mutant having a Asp to Lys substitution at residue 99

<400> 13

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu

1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly

20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala

35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr

50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln

65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe

85 90 95

Val Lys Lys Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg

100 105 110

Phe Asn

<210> 14

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; hIL13 mutant having a Leu to Ala substitution at residue 102

&lt;400&gt; 14

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Ala His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

&lt;210&gt; 15

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; hIL13 mutant having a Leu to Ala substitution at residue 104

&lt;400&gt; 15

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu

1            5            10            15  
 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
           20            25            30  
 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
           35            40            45  
 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
           50            55            60  
 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65            70            75            80  
 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
           85            90            95  
 Val Lys Asp Leu Leu Leu His Ala Lys Lys Leu Phe Arg Glu Gly Arg  
           100            105            110  
 Phe Asn

<210> 16  
 <211> 114  
 <212> PRT  
 <213> ARTIFICIAL SEQUENCE  
  
 <220>  
 <221> misc\_feature  
 <223> hIL13 mutant having a Lys to Asp substitution at residue 105

<400> 16

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1            5            10            15  
 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
           20            25            30  
 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
           35            40            45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Asp Lys Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 17

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<221> misc\_feature

<223> hIL13 mutant having a Lys to Asp substitution at residue 106

<400> 17

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Asp Leu Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 18

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<221> misc\_feature

<223> hIL13 mutant having a Leu to Ala substitution at residue 107

<400> 18

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Ala Phe Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 19

<211> 114  
 <212> PRT  
 <213> ARTIFICIAL SEQUENCE

<220>  
 <221> misc\_feature  
 <223> hIL13 mutant having a Phe to Tyr substitution at residue 108

<400> 19

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Tyr Arg Glu Gly Arg  
 100 105 110

Phe Asn

<210> 20  
 <211> 114  
 <212> PRT  
 <213> ARTIFICIAL SEQUENCE

<220>  
 <221> misc\_feature  
 <223> hIL13 mutant having a Arg to Asp substitution at residue 109



&lt;400&gt; 20

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Asp Glu Gly Arg  
 100 105 110

Phe Asn

&lt;210&gt; 21

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; hIL13 mutant having a Arg to Asp substitution at residue 112

&lt;400&gt; 21

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Asp  
 100 105 110

Phe Asn

<210> 22

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<221> misc\_feature

<223> hIL13 mutant having a Phe to Asp substitution at residue 113

<400> 22

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln

65            70            75            80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
           85            90            95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
           100            105            110

Asp Asn

<210> 23

<211> 114

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<221> misc\_feature

<223> hIL13 mutant having an Asn to Asp substitution at residue 113

<400> 23

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
   1            5            10            15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
           20            25            30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
           35            40            45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
           50            55            60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
   65            70            75            80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
           85            90            95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
           100            105            110

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.3	0	1
Smoking	0.2	0.4	0	1
Drinking	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.6	0.4	0	1
Sleep	0.7	0.3	0	1
Work	0.8	0.2	0	1
Family	0.9	0.1	0	1
Friends	0.7	0.4	0	1
Community	0.6	0.3	0	1
Society	0.5	0.5	0	1
Nature	0.4	0.4	0	1
Art	0.3	0.3	0	1
Music	0.2	0.2	0	1
Reading	0.1	0.1	0	1
Travel	0.05	0.05	0	1
Volunteering	0.02	0.02	0	1
Philosophy	0.01	0.01	0	1
Religion	0.005	0.005	0	1
Politics	0.001	0.001	0	1
Science	0.0005	0.0005	0	1
History	0.0001	0.0001	0	1
Language	0.00005	0.00005	0	1
Mathematics	0.00001	0.00001	0	1
Physics	0.000005	0.000005	0	1
Chemistry	0.000001	0.000001	0	1
Biology	0.0000005	0.0000005	0	1
Medicine	0.0000001	0.0000001	0	1
Law	0.00000005	0.00000005	0	1
Business	0.00000001	0.00000001	0	1
Engineering	0.000000005	0.000000005	0	1
Architecture	0.000000001	0.000000001	0	1
Design	0.0000000005	0.0000000005	0	1
Writing	0.0000000001	0.0000000001	0	1
Artistic	0.00000000005	0.00000000005	0	1
Creative	0.00000000001	0.00000000001	0	1
Innovative	0.000000000005	0.000000000005	0	1
Imaginative	0.000000000001	0.000000000001	0	1
Intuitive	0.0000000000005	0.0000000000005	0	1
Spiritual	0.0000000000001	0.0000000000001	0	1
Mystical	0.00000000000005	0.00000000000005	0	1
Esoteric	0.00000000000001	0.00000000000001	0	1
Occult	0.000000000000005	0.000000000000005	0	1
Paranormal	0.000000000000001	0.000000000000001	0	1
Unexplained	0.0000000000000005	0.0000000000000005	0	1
Mysterious	0.0000000000000001	0.0000000000000001	0	1
Enigmatic	0.00000000000000005	0.00000000000000005	0	1
Curious	0.00000000000000001	0.00000000000000001	0	1
Wonderful	0.000000000000000005	0.000000000000000005	0	1
Astonishing	0.000000000000000001	0.000000000000000001	0	1
Amazing	0.0000000000000000005	0.0000000000000000005	0	1
Incredible	0.0000000000000000001	0.0000000000000000001	0	1
Unbelievable	0.00000000000000000005	0.00000000000000000005	0	1
Remarkable	0.00000000000000000001	0.00000000000000000001	0	1
Outstanding	0.000000000000000000005	0.000000000000000000005	0	1
Exceptional	0.000000000000000000001	0.000000000000000000001	0	1
Extraordinary	0.0000000000000000000005	0.0000000000000000000005	0	1
Unprecedented	0.0000000000000000000001	0.0000000000000000000001	0	1
Unparalleled	0.00000000000000000000005	0.00000000000000000000005	0	1
Unsurpassed	0.00000000000000000000001	0.00000000000000000000001		